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                   Substances (PICCS) has been added to CHEMLIST
 NEWS  3  Oct 27   New Extraction Code PAX now available in Derwent
                   Files
 NEWS  4  Oct 27   SET ABBREVIATIONS and SET PLURALS extended in
                   Derwent World Patents Index files
 NEWS  5  Oct 27   Patent Assignee Code Dictionary now available
                   in Derwent Patent Files
 NEWS  6  Oct 27   Plasdoc Key Serials Dictionary and Echoing added to
                   Derwent Subscriber Files WPIDS and WPIX
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 NEWS  8  Dec  5   French Multi-Disciplinary Database PASCAL Now on STN
 NEWS  9  Dec  5   Trademarks on STN - New DEMAS and EUMAS Files
 NEWS 10  Dec 15   2001 STN Pricing
 NEWS 11  Dec 17   Merged CEABA-VTB for chemical engineering and
                   biotechnology
 NEWS 12  Dec 17   Corrosion Abstracts on STN
 NEWS 13  Dec 17   SYNTHLINE from Prous Science now available on STN
 NEWS 14  Dec 17   The CA Lexicon available in the CAPLUS and CA files
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=> file biosis, medlin[redacted]uspat, wpids, japio, jicst, fs[redacted] frosti

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=> s macadamia integrifolia

L1 222 MACADAMIA INTEGRIFOLIA

=> s l1 and (antimicrobial activity?)

L2 5 L1 AND (ANTIMICROBIAL ACTIVITY?)

=> d l2 ti abs ibib tot

L2 ANSWER 1 OF 5 BIOSIS COPYRIGHT 2001 BIOSIS
TI A family of antimicrobial peptides is produced by processing of a 7S globulin protein in **Macadamia integrifolia** kernels.
AB A new family of antimicrobial peptides has been discovered in **Macadamia integrifolia**. The first member of this new family to be purified from nut kernels was a peptide of 45 aa residues, termed MiAMP2c. This peptide inhibited various plant pathogenic fungi in vitro. cDNA clones corresponding to MiAMP2c encoded a 666 aa precursor protein homologous to vicilin 7S globulin proteins. The deduced precursor protein sequence contained a putative hydrophobic N-terminal signal sequence (28 aa), an extremely hydrophilic N-proximal region (212 aa), and a C-terminal region of 426 aa which is represented in all vicilins. The hydrophilic portion of the deduced protein contained the sequence for MiAMP2c as well as three additional segments having the same cysteine spacing pattern as MiAMP2c. Each member of the MiAMP2 family (i.e. MiAMP2a, b, c and d) consisted of approximately 50 amino acids and contained a C-X-X-X-C-(10-12)X-C-X-X-X-C motif. Subsequent isolations from seed exudates led to the purification of the predicted family members MiAMP2b and 2d, both of which also exhibited **antimicrobial activity** in vitro. These results suggest that some vicilins play a role in defence during seed germination.

ACCESSION NUMBER: 19[redacted]482584 BIOSIS
DOCUMENT NUMBER: PR[redacted]199900482584
TITLE: A family of antimicrobial peptides is produced by processing of a 7S globulin protein in **Macadamia integrifolia** kernels.
AUTHOR(S): Marcus, John P.; Green, Jodie L.; Goulter, Ken C.; Manners, John M. (1)
CORPORATE SOURCE: (1) Cooperative Research Centre for Tropical Plant Pathology, University of Queensland, Brisbane, QLD, 4072 Australia
SOURCE: Plant Journal, (Sept., 1999) Vol. 19, No. 6, pp. 699-710. ISSN: 0960-7412.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 2 OF 5 BIOSIS COPYRIGHT 2001 BIOSIS
TI Isolation and characterisation of antimicrobial proteins from Australian native plants.
AB We are currently screening Australian native plants for the presence of novel antimicrobial proteins. Proteins from the seeds of 200 plant accessions have been extracted and tested for **antimicrobial activity**. Several of these extracts exhibited significant inhibition against several plant pathogenic fungi. Two of these extracts were further purified to reveal two low molecular weight cysteine-rich peptides with potent **antimicrobial activity** toward a panel of phytopathogens. The first peptide isolated from Hardenbergia violacea (false sarsaparilla) was found to be a member of a previously characterised family of peptides known as plant defensins. This family has been isolated from numerous plant species and found to possess broad range potent **antimicrobial activity**. The second peptide was isolated from **Macadamia integrifolia**; comparisons with sequence databases indicated no homologies with any previously identified proteins. Although both of these peptides show strong inhibitory activity in vitro towards phytopathogens, they have shown no inhibitory, activity against the plant and animal cell lines tested.
ACCESSION NUMBER: 1999:218637 BIOSIS
DOCUMENT NUMBER: PREV199900218637
TITLE: Isolation and characterisation of antimicrobial proteins from Australian native plants.
AUTHOR(S): Harrison, Stuart J. (1); Marcus, John P. (1); Green, Jodie L. (1); Goulter, Ken C. (1); Maclean, Donald J. (1); Manners, John M. (1)
CORPORATE SOURCE: (1) Cooperative Research Centre for Tropical Plant Pathology, University of Queensland, Santa Lucia, 4072 Australia
SOURCE: Proceedings of the Royal Society of Queensland, (Sept. 11, 1998) Vol. 107, No. 0, pp. 119-121. ISSN: 0080-469X.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2001 BIOSIS
TI Purification, characterisation and cDNA cloning of an antimicrobial peptide from **Macadamia integrifolia**.
AB An antimicrobial peptide with no significant amino acid sequence similarity to previously described peptides has been isolated from the nut kernels of **Macadamia integrifolia**. The peptide, termed

MiAMP1, is highly basic with an estimated pI of 10 a mass of 8.1 kDa and contains 76 amino acids including 6 cysteine residues. A cDNA clone containing the entire coding region corresponding to the peptide was obtained. The deduced amino acid sequence of the cDNA indicated a 26-amino-acid signal peptide at the N-terminus of the preprotein. Purified MiAMP1 inhibited the growth of a variety of fungal, oomycete and gram-positive bacterial phytopathogens in vitro. Some pathogens exhibited close to 100% inhibition in less than 1 mu-M peptide (5 mu-g/ml). **Antimicrobial activity** was diminished against most, but not all, microbes in the presence of calcium and potassium chloride salts (1 mM and 50 mM, respectively). MiAMP1 was active against bakers yeast, was inactive against Escherichia coli and was non-toxic to plant and mammalian cells. Analysis of genomic DNA indicated that MiAMP1 was encoded on a single copy gene containing no introns. The MiAMP1 gene may prove useful in genetic manipulations to increase disease resistance in transgenic plants.

ACCESSION NUMBER: 1997:204101 BIOSIS
DOCUMENT NUMBER: PREV199799503304
TITLE: Purification, characterisation and cDNA cloning of an antimicrobial peptide from **Macadamia integrifolia**.
AUTHOR(S): Marcus, John P.; Goulter, Ken C.; Green, Jodie L.; Harrison, Stuart J.; Manners, John M. (1)
CORPORATE SOURCE: (1) Cooperative Res. Cent. Tropical Plant Pathol., John Hines Build., Univ. Queensland, Brisbane, QLD 4072 Australia
SOURCE: European Journal of Biochemistry, (1997) Vol. 244, No. 3, pp. 743-749.
ISSN: 0014-2956.
DOCUMENT TYPE: Article
LANGUAGE: English

L2 ANSWER 4 OF 5 MEDLINE
TI A family of antimicrobial peptides is produced by processing of a 7S globulin protein in **Macadamia integrifolia** kernels.
AB A new family of antimicrobial peptides has been discovered in **Macadamia integrifolia**. The first member of this new family to be purified from nut kernels was a peptide of 45 aa residues, termed MiAMP2c. This peptide inhibited various plant pathogenic fungi in vitro. cDNA clones corresponding to MiAMP2c encoded a 666 aa precursor protein homologous to vicilin 7S globulin proteins. The deduced precursor protein sequence contained a putative hydrophobic N-terminal signal sequence (28 aa), an extremely hydrophilic N-proximal region (212 aa), and a C-terminal region of 426 aa which is represented in all vicilins. The hydrophilic portion of the deduced protein contained the sequence for MiAMP2c as well as three additional segments having the same cysteine spacing pattern as MiAMP2c. Each member of the MiAMP2 family (i.e. MiAMP2a, b, c and d) consisted of approximately 50 amino acids and contained a C-X-X-X-C-(10-12)X-C-X-X-X-C motif. Subsequent isolations from seed exudates led to the purification of the predicted family members MiAMP2b and 2d, both of which also exhibited **antimicrobial activity** in vitro. These results suggest that some vicilins play a role in defence during seed germination.

ACCESSION NUMBER: 2000040040 MEDLINE
DOCUMENT NUMBER: 20040040
TITLE: A family of antimicrobial peptides is produced by processing of a 7S globulin protein in **Macadamia integrifolia** kernels.
AUTHOR: Marcus J P; Green J L; Goulter K C; Manners J M

CORPORATE SOURCE: Cooperative Research Centre for Tropical Plant Pathology, The University of Queensland, Brisbane, Australia.
SOURCE: PLANT JOURNAL, (1999 Sep) 19 (6) 699-710.
Journal code: BRU. ISSN: 0960-7412.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF161883; GENBANK-AF161884; GENBANK-AF161885
ENTRY MONTH: 200005
ENTRY WEEK: 20000504

L2 ANSWER 5 OF 5 MEDLINE
TI Purification, characterisation and cDNA cloning of an antimicrobial peptide from **Macadamia integrifolia**.
AB An antimicrobial peptide with no significant amino acid sequence similarity to previously described peptides has been isolated from the nut kernels of Macadcamia integrifolia. The peptide, termed MiAMP1, is highly basic with an estimated pI of 10.1, a mass of 8.1 kDa and contains 76 amino acids including 6 cysteine residues. A cDNA clone containing the entire coding region corresponding to the peptide was obtained. The deduced amino acid sequence of the cDNA indicated a 26-amino-acid signal peptide at the N-terminus of the preprotein. Purified MiAMP1 inhibited the growth of a variety of fungal, oomycete and gram-positive bacterial phytopathogens in vitro. Some pathogens exhibited close to 100% inhibition in less than 1 microM peptide (5 microg/ml). **Antimicrobial activity** was diminished against most, but not all, microbes in the presence of calcium and potassium chloride salts (1 mM and 50 mM, respectively). MiAMP1 was active against bakers yeast, was inactive against Escherichia coli and was non-toxic to plant and mammalian cells. Analysis of genomic DNA indicated that MiAMP1 was encoded on a single copy gene containing no introns. The MiAMP1 gene may prove useful in genetic manipulations to increase disease resistance in transgenic plants.
ACCESSION NUMBER: 97261828 MEDLINE
DOCUMENT NUMBER: 97261828
TITLE: Purification, characterisation and cDNA cloning of an antimicrobial peptide from **Macadamia integrifolia**.
AUTHOR: Marcus J P; Goulter K C; Green J L; Harrison S J; Manners J M
CORPORATE SOURCE: Cooperative Research Centre for Tropical Plant Pathology, The University of Queensland, Brisbane, Australia.
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1997 Mar 15) 244 (3) 743-9.
Journal code: EMZ. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
OTHER SOURCE: GENBANK-Y10903
ENTRY MONTH: 199707
ENTRY WEEK: 19970704

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FILE 'BIOSIS, MED[redacted]E, USPATFULL, WPIDS, JAPIO, JI -EPLUS, FSTA, FROSTI' ENTERED AT 16:31:29 ON 11 MAR 2001

L1 222 S MACADAMIA INTEGRIFOLIA
L2 5 S L1 AND (ANTIMICROBIAL ACTIVITY?)

=> s theobroma cacao

L3 1509 THEOBROMA CACAO

=> s l3 and vicilin

L4 29 L3 AND VICILIN

=> s l4 and (antimicrobial acitivity?)

L5 0 L4 AND (ANTIMICROBIAL ACITIVITY?)

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L4 ANSWER 1 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS

TI Identification and cloning of a complementary DNA encoding a **vicilin**-like proprotein, Jug r 2, from English walnut kernel (Juglans regia), a major food allergen.

AB Background: Walnuts and other tree nuts are important food-allergen sources that have the potential to be associated with life-threatening, IgE-mediated systemic reactions in some individuals. Objective: The purpose of this study was to characterize a complementary (c)DNA clone encoding one of the walnut food allergens. Methods: A cDNA expression library prepared from walnut somatic embryo was screened for IgE reactivity with patient serum. A reactive clone of 2060 bp, which encoded a protein of 593 amino acids in length, was subcloned by excision into the pGEX expression vector. IgE-binding inhibition experiments were performed.

Results: A recombinant fusion protein was induced and shown to bind serum IgE from 9 of 15 patients tested, thus identifying a major allergen. This clone, named Jug r 2, exhibited significant homology with genes encoding the **vicilin** group of seed proteins. An IgE-binding inhibition experiment suggested that the encoded protein undergoes posttranslational modification into at least one major polypeptide (47 kd) and possibly several others, which is similar to the **vicilin**-like proteins characterized in cocoa bean (**Theobroma cacao**) and cottonseed (Gossypium hirsutum). N-terminal sequencing of the 47-kd band, Jug r 2, identified it as a mature protein obtained from the precursor. A second IgE-binding inhibition experiment showed that there is minimal or no cross-reactivity between Jug r 2 and pea **vicilin**, peanut proteins, or cacao proteins. Conclusion: Jug r 2 is the third **vicilin** food allergen identified in addition to vicilins from soy and peanut. The availability of recombinant food allergens should help advance studies on the immunopathogenesis and possible treatment of IgE-mediated food hypersensitivity.

ACCESSION NUMBER: 2000:77644 BIOSIS
DOCUMENT NUMBER: PREV200000077644
TITLE: Identification and cloning of a complementary DNA encoding a **vicilin**-like proprotein, Jug r 2, from English walnut kernel (Juglans regia), a major food allergen.
AUTHOR(S): Teuber, Suzanne S. (1); Jarvis, Koren C.; Dandekar, Abhaya M.; Peterson, W. Rich; Ansari, Aftab A.
CORPORATE SOURCE: (1) Division of Rheumatology, Allergy and Clinical Immunology, School of Medicine, University of California, Davis, One Shields Ave, TB 192, Davis, CA USA

SOURCE: Journal of Allergy and Clinical Immunology, (Dec., 1999) Vol. 104, No. 6, pp. 1311-1320.
ISSN: 0091-6749.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L4 ANSWER 2 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS
TI Primary structure of 6.5k-arginine/glutamate-rich polypeptide from the seeds of sponge gourd (Luffa cylindrica.
AB The amino acid sequence of 6.5k-arginine/glutamate rich polypeptide (6.5k-AGRP) from the seeds of sponge gourd (Luffa cylindrica) has been determined. The 6.5k-AGRP consists of a 47-residue polypeptide chain containing two disulfide bonds, and a molecular mass calculated to be 5695
Da, which fully coincides with a value of (M + H)+ = m/z 5693.39 obtained by matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF MS). The mass spectrometric evidence indicated that 6.5k-AGRP is also present partially truncated at the C-terminus. In our preparations, approximately half of the polypeptide molecules have the
C-terminal sequence Arg-Arg-Glu-Val-Asp; the other half lack Val-Asp and end with the glutamic acid, making a total of 45 residues in the polypeptide chain. The two disulfide bonds connect Cys-12 to Cys-33 and Cys-16 to Cys-29. Comparison of the amino acid sequence of 6.5k-AGRP with those of the other known proteins included in the PIR protein sequence database showed that it is related to the amino acid sequence of the N-terminal region encoded by the first exon of the cocoa (Theohroma cacao)
and cotton seeds **vicilin** genes, sharing a characteristic two Cys-Xaa-Xaa-Xaa-Cys motif.
ACCESSION NUMBER: 1997:415187 BIOSIS
DOCUMENT NUMBER: PREV199799707230
TITLE: Primary structure of 6.5k-arginine/glutamate-rich polypeptide from the seeds of sponge gourd (Luffa cylindrica.
AUTHOR(S): Kimura, Makoto (1); Park, Sung-Soo (1); Sakai, Ritsu (1); Yamasaki, Nobuyuki (1); Funatsu, Gunki
CORPORATE SOURCE: (1) Lab. Biochem., Fac. Agric., Kyushu Univ., Fukuoka 812-81 Japan
SOURCE: Bioscience Biotechnology and Biochemistry, (1997) Vol. 61, No. 6, pp. 984-988.
ISSN: 0916-8451.
DOCUMENT TYPE: Article
LANGUAGE: English

L4 ANSWER 3 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS
TI Phylogenetic relationships of chocolate and its wild relatives based on sequence data from the nuclear gene **vicilin**.
ACCESSION NUMBER: 1997:374417 BIOSIS
DOCUMENT NUMBER: PREV199799673620
TITLE: Phylogenetic relationships of chocolate and its wild relatives based on sequence data from the nuclear gene **vicilin**.
AUTHOR(S): Whitlock, Barbara A..; Baum, David A.
CORPORATE SOURCE: Dep. Organismic Evolutionary Biol., Harvard Univ., Cambridge, MA 02138 USA
SOURCE: American Journal of Botany, (1997) Vol. 84, No. 6 SUPPL., pp. 244.
Meeting Info.: Meeting of the Botanical Society of America and the Canadian Botanical Association/Association Botanique du Canada Montreal, Quebec, Canada August 3-7, 1997

ISSN: 0002-9122.
DOCUMENT TYPE: Conference; Abstract
LANGUAGE: English

L4 ANSWER 4 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS
TI Formation of cocoa-specific aroma precursors by proteolysis of a **vicilin**-like storage protein of cocoa seeds.
ACCESSION NUMBER: 1996:345745 BIOSIS
DOCUMENT NUMBER: PREV199699068101
TITLE: Formation of cocoa-specific aroma precursors by proteolysis of a **vicilin**-like storage protein of cocoa seeds.
AUTHOR(S): Voigt, Juergen; Heinrichs, Heinrich; Voigt, Gesine; Bytof, Gerhard; Biehl, Boele
CORPORATE SOURCE: Bot. Inst. Bot. Garten, Technische Univ. Braunschweig, Braunschweig Germany
SOURCE: CIRAD.. (1995) pp. 213. Cocoa meetings: The various aspects of quality.
Publisher: CIRAD (Centre de Cooperation Internationale en Recherche Agronomique pour le Developpement) Montpellier, France.
Meeting Info.: Seminar Proceedings Montpellier, France June 30, 1995
ISBN: 2-87614-224-4.
DOCUMENT TYPE: Book; Conference
LANGUAGE: English

L4 ANSWER 5 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS
TI Expression of the major bean proteins from **Theobroma cacao** (cocoa) in the yeasts Hansenula polymorpha and Saccharomyces cerevisiae.
AB The production in two yeast expression systems of recombinant forms of the major proteins from the cocoa bean is described. Three major protein species are found in the cocoa bean: an albumin of molecular mass 21 kDa (p21) and two insoluble **vicilin**-like proteins of molecular mass 31 kDa and 47 kDa (p31 and p47, respectively). The p31 and p47 species are known to be derived from a common 67-kDa precursor (p67) by post-translational processing that includes the deletion of a hydrophilic domain located immediately after an N-terminal signal sequence. All three proteins appear to be targeted to membrane-bound storage organelles by N-terminal signal sequences. The p21 and p67 coding sequences were expressed in Hansenula polymorpha using the powerful methanol oxidase (MOX) promoter and in Saccharomyces cerevisiae using the promoter of the pyruvate kinase (PYK) gene. The expression constructs contained the native plant signal sequence, or the appearance of other protein species.
ACCESSION NUMBER: 1996:242290 BIOSIS
DOCUMENT NUMBER: PREV199698790419
TITLE: Expression of the major bean proteins from **Theobroma cacao** (cocoa) in the yeasts Hansenula polymorpha and Saccharomyces cerevisiae.
AUTHOR(S): Yavuz, M. O.; Ashton, S. M. V.; Deakin, E. D.; Spencer, M. E.; Sudbery, P. E. (1)
CORPORATE SOURCE: (1) Dep. Molecular Biol. Biotechnol., Univ. Sheffield, Western Bank, Sheffield S10 2TN UK
SOURCE: Journal of Biotechnology, (1996) Vol. 46, No. 1, pp. 43-54.
ISSN: 0168-1656.
DOCUMENT TYPE: Article

LANGUAGE: English

L4 ANSWER 6 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS
TI A model for **vicilin** solubility at mild acidic pH, based on homology modelling and electrostatics calculations.
AB The crystallographic structures of jack bean canavalin and French bean phaseolin have been used to construct a homology model of the storage **vicilin** of cocoa. Reported molecular weights for cocoa storage protein subunits correlate with proteolysis at the site of a large hydrophilic insert in the mature protein. Burial of the hydrophobic amino acids on trimer formation is a strongly conserved feature in the **vicilin** family. Histidine residues also sit at the monomer-monomer interfaces of the trimer and are likely to contribute to the decreased solubility of cocoa **vicilin** at mild acidic pH, which is generally considered to be caused solely by aggregation near to the isoelectric point. Electrostatic calculations suggest that such an arrangement of histidine residues in the absence of specific counterion binding will not favour the particular geometry of trimer formation below neutral pH. Higher order aggregates that do not exclude histidine charge from the solvent may be favoured, aiding the precipitation of cocoa **vicilin** at mild acidic pH. This suggestion is considered for the **vicilin** family. The hypothesis could contribute to an understanding of the pH and ionic strength dependence of **vicilin** solubility in vitro, and possibly of the behaviour of vicilins in the seed storage environment.
ACCESSION NUMBER: 1996:233286 BIOSIS
DOCUMENT NUMBER: PREV199698797415
TITLE: A model for **vicilin** solubility at mild acidic pH, based on homology modelling and electrostatics calculations.
AUTHOR(S): Warwicker, J. (1); O'Connor, J.
CORPORATE SOURCE: (1) Protein Eng. Dep., Inst. Food Res., Reading Lab., Earley Gate, Whiteknights Road, Reading RG6 6BZ UK
SOURCE: Protein Engineering, (1995) Vol. 8, No. 12, pp. 1243-1251.
ISSN: 0269-2139.
DOCUMENT TYPE: Article
LANGUAGE: English

L4 ANSWER 7 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS
TI Legumin-like and **vicilin**-like seed storage proteins: Evidence for a common single-domain ancestral gene.
AB Legumin-like 11S and **vicilin**-like 7S globulins are the main storage proteins of most angiosperms and gymnosperms. The subunits of the hexameric legumin are synthesized as a precursor comprising a N-terminal acidic alpha- and a C-terminal basic beta-chain. The trimeric **vicilin** molecule consists of subunits composed of two symmetrical N- and C-terminal structural domains. In a multiple alignment we have compared the N-terminal and C-terminal domains of 11 legumins and seven vicilins of several dicot, monocot, and gymnosperm species. The comparisons using all six possible pairwise combinations reveal that the N-terminal and C-terminal domains of both protein families are similar to each other. These results together with data on the distribution of variable and conserved regions, on the positions of susceptible sites for proteolytic attack, as well as on the published 7S protein tertiary structure suggest that both protein families share a common single-domain ancestor molecule and lead to the hypothesis that a triplication event has occurred during the evolution of a putative legumin/**vicilin** ancestor gene. Moreover, the comparison of the intron/exon pattern reveals that at least three out of five intron positions are precisely conserved

between the genes of both protein families, furthe upporting the idea of
a common evolutionary origin of recent legumin and **vicilin** encoding genes.

ACCESSION NUMBER: 1996:76718 BIOSIS
DOCUMENT NUMBER: PREV199698648853
TITLE: Legumin-like and **vicilin**-like seed storage proteins: Evidence for a common single-domain ancestral gene.
AUTHOR(S): Shutov, A. D.; Kakhovskaya, I. A.; Braun, H.; Baumlein, H. (1); Muentz, K.
CORPORATE SOURCE: (1) Inst. Plant Genet., Crop Plant Res., Correnssstr. 3, D-06466 Gatersleben Germany
SOURCE: Journal of Molecular Evolution, (1995) Vol. 41, No. 6, pp. 1057-1069.
ISSN: 0022-2844.
DOCUMENT TYPE: Article
LANGUAGE: English

L4 ANSWER 8 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS
TI The major seed proteins of **Theobroma cacao** L.
AB Differential extractions of proteins from **Theobroma cacao** seeds have revealed the presence of an albumin fraction and a globulin fraction with proportions of 52% and 43%, respectively, of total seed proteins. In contrast to some earlier reports, we could not detect any prolamin. The 'glutelin fraction' described in the literature was found to consist of residual globulin. After fermentation, the first step in cocoa processing, the proportion of the globulin fraction is considerably reduced. The major albumin is a polypeptide with an apparent molecular weight of 19 kDa. The globulin fraction contained polypeptides with apparent molecular sizes of 47 kDa, 31 kDa, and 14.5 ka. Globulin prepared in the absence of the aspartyl protease inhibitor pepstatin contained two additional polypeptides with apparent molecular sizes of 28 kDa and 16 kDa, respectively. The negative globulin on **Theobroma cacao** is a glycoprotein with a sedimentation coefficient of 7-8S and a molecular weight of 150 kDa. Its subunits are not cross-linked by disulphide bridges-in contrast to the legumin-like storage globulins which are predominant in the seeds of all other dicotyledons studied so far. Therefore, **Theobroma cacao** is the first plant described to date whose seeds contain a **vicilin**-like globulin, but apparently no legumin-class globulin.

ACCESSION NUMBER: 1993:319105 BIOSIS
DOCUMENT NUMBER: PREV199396027455
TITLE: The major seed proteins of **Theobroma cacao** L.
AUTHOR(S): Voigt, Juergen (1); Biehl, Bole; Wazir, Syed Kamaruddin Syed
CORPORATE SOURCE: (1) Botanisches Institut der Technischen Universitaet Braunschweig, Mendelssohnstrasse 4, W-3300 Branschweig Germany
SOURCE: Food Chemistry, (1993) Vol. 47, No. 2, pp. 145-151.
ISSN: 0308-8146.
DOCUMENT TYPE: Article
LANGUAGE: English

L4 ANSWER 9 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS
TI COMPARISON OF THE STRUCTURE AND NUCLEOTIDE SEQUENCES OF **VICILIN** GENES OF COCOA AND COTTON RAISE QUESTIONS ABOUT **VICILIN** EVOLUTION.

ACCESSION NUMBER: 1992:376484 BIOSIS
DOCUMENT NUMBER: BR43:43434
TITLE: COMPARISON OF THE STRUCTURE AND NUCLEOTIDE SEQUENCES OF

VICI[redacted] GENES OF COCOA AND COTTON RAI[redacted] QUESTIONS ABO[redacted] **VICILIN** EVOLUTION.
AUTHOR(S): MCHENRY L; FRITZ P J
CORPORATE SOURCE: DEP. FOOD SCIENCE INTERCOLLEGE PLANT PHYSIOLOGY PROGRAM, PENNSYLVANIA STATE UNIVERSITY, 215 BORLAND LABORATORY, UNIVERSITY PARK, PA. 16802, USA.
SOURCE: Plant Mol. Biol., (1992) 18 (6), 1173-1176.
CODEN: PMBIDB. ISSN: 0167-4412.
FILE SEGMENT: BR; OLD
LANGUAGE: English

L4 ANSWER 10 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS
TI MOLECULAR MARKERS FOR GENETIC ANALYSIS OF **THEOBROMA-CACAO**.
ACCESSION NUMBER: 1992:336435 BIOSIS
DOCUMENT NUMBER: BR43:25985
TITLE: MOLECULAR MARKERS FOR GENETIC ANALYSIS OF **THEOBROMA -CACAO**.
AUTHOR(S): OSEI J K; FRITZ P J
CORPORATE SOURCE: ACRI-COCOA MOLECULAR BIOL. LAB., FOOD SCI. DEP., PENN STATE
UNIV., UNIVERSITY PARK, PA. 16802.
SOURCE: KEYSTONE SYMPOSIUM ON CROP IMPROVEMENT VIA BIOTECHNOLOGY: AN INTERNATIONAL PERSPECTIVE, KEYSTONE, COLORADO, USA, APRIL 10-16, 1992. J CELL BIOCHEM SUPPL, (1992) 0 (16 PART F), 220.
CODEN: JCBSD7.
DOCUMENT TYPE: Conference
FILE SEGMENT: BR; OLD
LANGUAGE: English

L4 ANSWER 11 OF 29 BIOSIS COPYRIGHT 2001 BIOSIS
TI CLONING AND SEQUENCING OF A CDNA ENCODING THE MAJOR STORAGE PROTEINS OF **THEOBROMA-CACAO** IDENTIFICATION OF THE PROTEINS AS MEMBERS OF THE **VICILIN** CLASS OF STORAGE PROTEINS.
AB The major storage proteins, polypeptides of 31 and 47 kilodaltons (kDa), from the seeds of cocoa (**Theobroma cacao** L.), have been identified and partially purified by preparative gel electrophoresis.
The polypeptides were both N-terminally blocked, but some N-terminal amino-acid sequence was obtained from a cyanogen bromide peptide common to both polypeptides, permitting the construction of an oligonucleotide probe. This probe was used to isolate the corresponding copy-DNA (cDNA) clone from a library made from poly(A)+RNA from immature cocoa beans. The cDNA sequence has a single major open reading frame, that translates to give a 566-amino-acid polypeptide of Mr 65612. The existence of a common precursor to the 31- and 47-kDa polypeptides of this size was confirmed by immunoprecipitation from total poly(A)+RNA translation products. The precursor has an N-terminal hydrophobic sequence which appears to be a typical signal sequence, with a predicted site of cleavage 20 amino acids after the start. This is followed by a very hydrophilic domain of .apprx. 110 amino acids, which, by analogy with the cottonseed .alpha.-globulin, is presumed to be cleaved off to leave a domain of approx. 47 kDa, very close to the observed size of the mature polypeptide. Like the hydrophilic domain of the cottonseed .alpha.-globulin the cocoa hydrophilic domain is very rich in glutamine and charged residues (especially glutamate), and contains several Cys-X-X-X-Cys motifs. The cyanogen-bromide peptide common to the 47-kDa and 31-kDa polypeptides is very close to the proposed start

of the mature dom[redacted], indicating that the 31-kDa p[redacted]ypeptide arises via further C-termina[redacted]processing. The polypeptide seq[redacted]nce is homologous to sequences of the **vicilin** class of storage proteins, previously found only in legumes and cotton. Most of these proteins have a mature polypeptide size of approx. 47 kDa, and are synthesized as precursors only slightly larger than this. Some, however, are larger polypeptide (e.g. .alpha.-conglycinin from soybean is 72 kDa), usually due to an additional N-terminal domain. In cottonseed the situation appears to parallel that in cocoa in that the **vicilin** is synthesised as an approx. 70-kDa precursor and then processed to a 47-kDa (and in the case of cocoa also a 31-kDa) mature protein. In this context it is interesting that cotton is closer in evolutionary terms to cocoa than are the legumes, both cotton and cocoa being in the order Malvales.

ACCESSION NUMBER: 1992:257901 BIOSIS
DOCUMENT NUMBER: BA93:134226
TITLE: CLONING AND SEQUENCING OF A CDNA ENCODING THE MAJOR STORAGE PROTEINS OF **THEOBROMA-CACAO** IDENTIFICATION OF THE PROTEINS AS MEMBERS OF THE **VICILIN** CLASS OF STORAGE PROTEINS.
AUTHOR(S): SPENCER M E; HODGE R
CORPORATE SOURCE: PLANT SCI. LTD., FIRTH COURT, SHEFFIELD UNIV., WESTERN BANK, SHEFFIELD S10 2TN, UK.
SOURCE: PLANTA (HEIDELB), (1992) 186 (4), 567-576. CODEN: PLANAB. ISSN: 0032-0935.
FILE SEGMENT: BA; OLD
LANGUAGE: English

L4 ANSWER 12 OF 29 MEDLINE
TI Identification and cloning of a complementary DNA encoding a **vicilin**-like proprotein, jug r 2, from english walnut kernel (Juglans regia), a major food allergen.
AB BACKGROUND: Walnuts and other tree nuts are important food-allergen sources that have the potential to be associated with life-threatening, IgE-mediated systemic reactions in some individuals. OBJECTIVE: The purpose of this study was to characterize a complementary (c)DNA clone encoding one of the walnut food allergens. METHODS: A cDNA expression library prepared from walnut somatic embryo was screened for IgE reactivity with patient serum. A reactive clone of 2060 bp, which encoded a protein of 593 amino acids in length, was subcloned by excision into the pGEX expression vector. IgE-binding inhibition experiments were performed.
RESULTS: A recombinant fusion protein was induced and shown to bind serum IgE from 9 of 15 patients tested, thus identifying a major allergen. This clone, named Jug r 2, exhibited significant homology with genes encoding the **vicilin** group of seed proteins. An IgE-binding inhibition experiment suggested that the encoded protein undergoes posttranslational modification into at least one major polypeptide (47 kd) and possibly several others, which is similar to the **vicilin**-like proteins characterized in cocoa bean (**Theobroma cacao**) and cottonseed (Gossypium hirsutum). N-terminal sequencing of the 47-kd band, Jug r 2, identified it as a mature protein obtained from the precursor. A second IgE-binding inhibition experiment showed that there is minimal or no cross-reactivity between Jug r 2 and pea **vicilin**, peanut proteins, or cacao proteins. CONCLUSION: Jug r 2 is the third **vicilin** food allergen identified in addition to vicilins from soy and peanut. The availability of recombinant food allergens should help advance studies on the immunopathogenesis and possible treatment of IgE-mediated food hypersensitivity.
ACCESSION NUMBER: 2000057824 MEDLINE

DOCUMENT NUMBER: 20007824
TITLE: Identification and cloning of a complementary DNA encoding a **vicilin**-like proprotein, jug r 2, from english walnut kernel (Juglans regia), a major food allergen.
AUTHOR: Teuber S S; Jarvis K C; Dandekar A M; Peterson W R; Ansari A A
CORPORATE SOURCE: Division of Rheumatology, Allergy and Clinical Immunology, Department of Internal Medicine, University of California, Davis, School of Medicine, Davis, CA 95616, USA.
CONTRACT NUMBER: DK35747 (NIDDK)
SOURCE: JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY, (1999 Dec) 104 (6) 1311-20.
Journal code: H53. ISSN: 0091-6749.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
OTHER SOURCE: GENBANK-AF066055
ENTRY MONTH: 200003
ENTRY WEEK: 20000303

L4 ANSWER 13 OF 29 MEDLINE
TI Primary structure of 6.5k-arginine/glutamate-rich polypeptide from the seeds of sponge gourd (Luffa cylindrica).
AB The amino acid sequence of 6.5k-arginine/glutamate rich polypeptide (6.5k-AGRP) from the seeds of sponge gourd (Luffa cylindrica) has been determined. The 6.5k-AGRP consists of a 47-residue polypeptide chain containing two disulfide bonds, and a molecular mass calculated to be 5695
Da, which fully coincides with a value of [M+H]+ = m/zeta 5693.39 obtained
by matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF MS). The mass spectrometric evidence indicated that 6.5k-AGRP is also present partially truncated at the C-terminus. In our preparations, approximately half of the polypeptide molecules have the
C-terminal sequence Arg-Arg-Glu-Val-Asp; the other half lack Val-Asp and end with the glutamic acid, making a total of 45 residues in the polypeptide chain. The two disulfide bonds connect Cys12 to Cys33 and Cys16 to Cys29. Comparison of the amino acid sequence of 6.5k-AGRP with those of the other known proteins included in the PIR protein sequence database showed that it is related to the amino acid sequence of the N-terminal region encoded by the first exon of the cocoa (**Theobroma cacao**) and cotton seeds **vicilin**
genes, sharing a characteristic two Cys-Xaa-Xaa-Xaa-Cys motif.
ACCESSION NUMBER: 97357433 MEDLINE
DOCUMENT NUMBER: 97357433
TITLE: Primary structure of 6.5k-arginine/glutamate-rich polypeptide from the seeds of sponge gourd (Luffa cylindrica).
AUTHOR: Kimura M; Park S S; Sakai R; Yamasaki N; Funatsu G
CORPORATE SOURCE: Laboratory of Biochemistry, Faculty of Agriculture, Kyushu University, Fukuoka, Japan.
SOURCE: BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, (1997 Jun) 61 (6) 984-8.
Journal code: BDP. ISSN: 0916-8451.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; B
ENTRY MONTH: 199711

L4 ANSWER 14 OF 29 MEDLINE

TI Expression of the major bean proteins from **Theobroma cacao** (cocoa) in yeasts Hansenula polymorpha and Saccharomyces cerevisiae.

AB The production in two yeast expression systems of recombinant forms of the major proteins from the cocoa bean is described. Three major protein species are found in the cocoa bean: an albumin of molecular mass 21 kDa (p21) and two insoluble **vicilin**-like proteins of molecular mass 31 kDa and 47 kDa (p31 and p47, respectively). The p31 and p47 species are known to be derived from a common 67-kDa precursor (p67) by post-translational processing that includes the deletion of a hydrophilic domain located immediately after an N-terminal signal sequence. All three proteins appear to be targeted to membrane-bound storage organelles by N-terminal signal sequences. The p21 and p67 coding sequences were expressed in Hansenula polymorpha using the powerful methanol oxidase (MOX) promoter and in Saccharomyces cerevisiae using the promoter of the pyruvate kinase (PYK) gene. The expression constructs contained the native plant signal sequence, or various yeast signals. The p21 protein was successfully expressed and secreted from both yeasts. The insoluble p67 protein proved more difficult. Species of the correct molecular mass were recovered internally and small amounts of a p47 species were secreted using a yeast leader sequence. However, proteolytic cleavage, probably due to Kex2p-like processing, led to the appearance of other protein species.

ACCESSION NUMBER: 96273216 MEDLINE
DOCUMENT NUMBER: 96273216
TITLE: Expression of the major bean proteins from **Theobroma cacao** (cocoa) in the yeasts Hansenula polymorpha and Saccharomyces cerevisiae.
AUTHOR: Yavuz M O; Ashton S M; Deakin E D; Spencer M E; Sudbery P E
CORPORATE SOURCE: Department of Molecular Biology and Biotechnology, University of Sheffield, UK.
SOURCE: JOURNAL OF BIOTECHNOLOGY, (1996 Apr 18) 46 (1) 43-54. Journal code: AL6. ISSN: 0168-1656.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; B
ENTRY MONTH: 199610

L4 ANSWER 15 OF 29 USPATFULL

TI Nucleotide sequences of canola and soybean palmitoyl-ACP thioesterase genes and their use in the regulation of fatty acid content of the oils of soybean and canola plants

AB The preparation and use of nucleic acid fragments encoding acyl-acyl carrier protein thioesterase enzymes to modify plant lipid composition are disclosed. Also disclosed are chimeric genes incorporating such nucleic acid fragments and suitable regulatory sequences may be used to create transgenic plants with altered levels of saturated fatty acids.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 1999:113935 USPATFULL
TITLE: Nucleotide sequences of canola and soybean palmitoyl-ACP thioesterase genes and their use in the regulation of fatty acid content of the oils of soybean and canola plants
INVENTOR(S): Hitz, William Dean, Wilmington, DE, United States
PATENT ASSIGNEE(S): E. I. du Pont de Nemours and Company, Wilmington, DE, United States (U.S. corporation)

	NUMBER	DATE	
PATENT INFORMATION:	US 5955650	19990921	
	WO 9606936	19960307	
APPLICATION INFO.:	US 1997-793410	19970225	(8)
	WO 1995-US10627	19950825	
		19970224	PCT 371 date
		19970224	PCT 102(e) date

RELATED APPLN. INFO.: Continuation of Ser. No. US 1994-299044, filed on 31 Aug 1994, now abandoned
DOCUMENT TYPE: Utility
PRIMARY EXAMINER: Smith, Lynette F.
ASSISTANT EXAMINER: Nelson, Amy J.
NUMBER OF CLAIMS: 33
EXEMPLARY CLAIM: 1,12,24
LINE COUNT: 2939
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 16 OF 29 USPATFULL
TI Fatty acid desaturase genes from plants
AB The preparation and use of nucleic acid fragments encoding fatty acid desaturase enzymes are described. The invention permits alteration of plant lipid composition. Chimeric genes incorporating such nucleic acid fragments with suitable regulatory sequences may be used to create transgenic plants with altered levels of unsaturated fatty acids.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 1999:110533 USPATFULL
TITLE: Fatty acid desaturase genes from plants
INVENTOR(S): Browse, John, Palouse, WA, United States
Grau, Luis Perez, Davis, CA, United States
Kinney, Anthony J., Wilmington, DE, United States
Pierce, Jr., John W., Wilmington, DE, United States
Wierzbicki, Anna M., Wilmington, DE, United States
Yadav, Narendra S., Chadds Ford, PA, United States
PATENT ASSIGNEE(S): E. I. du Pont de Nemours and Company, Wilmington, DE, United States (U.S. corporation)

	NUMBER	DATE	
PATENT INFORMATION:	US 5952544	19990914	
	WO 9311245	19930610	
APPLICATION INFO.:	US 1994-244205	19940826	(8)
	WO 1992-US10284	19921203	
		19940826	PCT 371 date
		19940826	PCT 102(e) date

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1991-804259, filed on 4 Dec 1991, now abandoned
DOCUMENT TYPE: Utility
PRIMARY EXAMINER: McElwain, Elizabeth F.
NUMBER OF CLAIMS: 14
EXEMPLARY CLAIM: 1
LINE COUNT: 4676
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 17 OF 29 USPATFULL
TI Specific for palmitoyl, stearoyl and oleoyl-alp thioesters nucleic acid fragments encoding acyl-acp thiosesterase enzymes and the use of these fragments in altering plant oil composition
AB Isolated nucleic acid fragments encoding an acyl-ACP thioesterase enzyme
which catalyzes the hydrolysis of palmitoyl, stearoyl and oleoyl-ACP

thioesters are described. Use of such fragments altering plant oil composition is also described.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 1999:102974 USPATFULL
TITLE: Specific for palmitoyl, stearoyl and oleoyl-alp thioesters nucleic acid fragments encoding acyl-acp thiosesterase enzymes and the use of these fragments in altering plant oil composition
INVENTOR(S): Hitz, William Dean, Wilmington, DE, United States
Yadav, Narendra S., Chadds Ford, PA, United States
PATENT ASSIGNEE(S): E. I. du Pont de Nemours and Company, Wilmington, DE, United States (U.S. corporation)

	NUMBER	DATE	
PATENT INFORMATION:	US 5945585	19990831	
APPLICATION INFO.:	US 1997-948176	19971009	(8)
RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. US 1995-570925, filed on 12 Dec 1995, now abandoned which is a continuation-in-part of Ser. No. US 1993-75533, filed on 14 Jun 1993, now patented, Pat. No. US 5530186 which is a continuation-in-part of Ser. No. US 1990-631264, filed on 20 Dec 1990, now abandoned		

DOCUMENT TYPE: Utility
PRIMARY EXAMINER: Smith, Lynette F.
ASSISTANT EXAMINER: Nelson, Amy J.
NUMBER OF CLAIMS: 18
EXEMPLARY CLAIM: 1,17
LINE COUNT: 3734
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 18 OF 29 USPATFULL
TI Recombinant 47 and 31KD cocoa proteins and precursor
AB 47 kD and 31 kD proteins, and their 67 kD expression precursor, believed to be the source of peptide flavour precursors in cocoa (**Theobroma cacao**) have been identified. Genes coding for them have been probed, identified and sequenced, and recombinant proteins have been synthesised.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 1998:72465 USPATFULL
TITLE; Recombinant 47 and 31KD cocoa proteins and precursor
INVENTOR(S): Spencer, Margaret Elizabeth, Sheffield, England
Hodge, Rachel, Leicester, England
Deakin, Edward Alfred, Sheffield, England
Ashton, Sean, Sheffield, England
PATENT ASSIGNEE(S): Mars U.K. Limited, Berkshire, England (non-U.S. corporation)

	NUMBER	DATE	
PATENT INFORMATION:	US 5770433	19980623	
	WO 9119801	19911226	
APPLICATION INFO.:	US 1993-955905	19930121	(7)
	WO 1991-GB914	19910607	
		19930121	PCT 371 date
		19930121	PCT 102(e) date

NUMBER DATE

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PRIORITY INFORMATION:	GB 1990-13016	19900611
DOCUMENT TYPE:	Utility	
PRIMARY EXAMINER:	Spector, Lorraine M.	
LEGAL REPRESENTATIVE:	Santisi, Leonard J.	
NUMBER OF CLAIMS:	14	
EXEMPLARY CLAIM:	1	
NUMBER OF DRAWINGS:	22 Drawing Figure(s); 22 Drawing Page(s)	
LINE COUNT:	1351	

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 19 OF 29 USPATFULL

TI Nucleotide sequence of soybean stearoyl-ACP desaturase gene

AB The preparation and use of nucleic acid fragments encoding soybean seed stearoyl-ACP desaturase enzyme or its precursor to modify plant oil composition are described. Chimeric genes incorporating such nucleic acid fragments and suitable regulatory sequences may be utilized to transform plants to control the levels of saturated and unsaturated fatty acids.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	1998:61819 USPATFULL	
TITLE:	Nucleotide sequence of soybean stearoyl-ACP desaturase gene	
INVENTOR(S):	Hitz, William D., Wilmington, DE, United States Yadav, Narendra S., Wilmington, DE, United States Perez-Grau, Luis, Wilmington, DE, United States	
PATENT ASSIGNEE(S):	E. I. du Pont de Nemours and Company, Wilmington, DE, United States (U.S. corporation)	
	NUMBER	DATE
	----------	--------
PATENT INFORMATION:	US 5760206	19980602
APPLICATION INFO.:	US 1995-474587	19950607 (8)
RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. US 1992-995657, filed on 11 Dec 1992, now patented, Pat. No. US 5443974	
DOCUMENT TYPE:	Utility	
PRIMARY EXAMINER:	Benzion, Gary	
NUMBER OF CLAIMS:	5	
EXEMPLARY CLAIM:	1	
LINE COUNT:	2242	

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 20 OF 29 USPATFULL

TI Nucleotide sequences of soybean acyl-ACP thioesterase genes

AB The preparation and use of nucleic acid fragments encoding soybean seed acyl-ACP thioesterase enzyme or its precursor to modify plant oil composition are described. Chimeric genes incorporating such nucleic acid fragments and suitable regulatory sequences may be used to transform plants to control the levels of saturated and unsaturated fatty acids.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	96:55940 USPATFULL	
TITLE:	Nucleotide sequences of soybean acyl-ACP thioesterase genes	
INVENTOR(S):	Hitz, William D., Wilmington, DE, United States Yadav, Narendra S., Wilmington, DE, United States	
PATENT ASSIGNEE(S):	E. I. Du Pont de Nemours and Company, Wilmington, DE, United States (U.S. corporation)	
	NUMBER	DATE
	----------	--------

PATENT INFORMATION:	US 5530186	19960625	
	WO 9211373	19920907	
APPLICATION INFO.:	US 1993-75533	19930614	(8)
	WO 1991-US9160	19911216	
		19930614	PCT 371 date
		19930614	PCT 102(e) date

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1990-631264, filed on 20 Dec 1990, now abandoned
DOCUMENT TYPE: Utility
PRIMARY EXAMINER: Moody, Patricia R.
NUMBER OF CLAIMS: 20
EXEMPLARY CLAIM: 1
LINE COUNT: 2817
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 21 OF 29 USPATFULL
TI .beta.-ketoacyl-ACP synthetase II genes from plants
AB The preparation and use of nucleic acid fragments encoding .beta.-ketoacyl-ACP synthetase II enzyme or its precursor to modify plant oil composition are described. Chimeric genes incorporating such nucleic acid fragments and suitable regulatory sequences may be used to transform plants to control the levels of saturated and unsaturated fatty acids. Plants transformed with the chimeric genes, seeds and oil of such plants are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 96:23044 USPATFULL
TITLE: .beta.-ketoacyl-ACP synthetase II genes from plants
INVENTOR(S): Kinney, Anthony J., Wilmington, DE, United States
PATENT ASSIGNEE(S): E. I. Du Pont de Nemours and Company, Wilmington, DE, United States (U.S. corporation)

	NUMBER	DATE	
PATENT INFORMATION:	US 5500361	19960319	
	WO 9310240	19930527	
APPLICATION INFO.:	US 1994-232079	19940510	(8)
	WO 1992-US9733	19921112	
		19940510	PCT 371 date
		19940510	PCT 102(e) date

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1991-791921, filed on 15 Nov 1991, now abandoned
DOCUMENT TYPE: Utility
PRIMARY EXAMINER: Moody, Patricia R.
NUMBER OF CLAIMS: 10
EXEMPLARY CLAIM: 1
LINE COUNT: 2377
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 22 OF 29 USPATFULL
TI Nucleotide sequence of soybean stearoyl-ACP desaturase gene
AB The preparation and use of nucleic acid fragments encoding soybean seed stearoyl-ACP desaturase enzyme or its precursor to modify plant oil composition are described. Chimeric genes incorporating such nucleic acid fragments and suitable regulatory sequences may be utilized to transform plants to control the levels of saturated and unsaturated fatty acids.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 95:75885 USPATFULL
TITLE: Nucleotide sequence of soybean stearoyl-ACP desaturase gene
INVENTOR(S): Hitz, William D., Wilmington, DE, United States

PATENT ASSIGNEE(S): Yadav, Narendra S., Wilmington, DE, United States
Perez-Grau, Luis, Wilmington, DE, United States
E. I. Du Pont de Nemours and Company, Wilmington, DE, United States (U.S. corporation)

	NUMBER	DATE
PATENT INFORMATION:	US 5443974	19950822
APPLICATION INFO.:	US 1992-995657	19921211 (7)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1990-529049, filed on 25 May 1990, now abandoned
DOCUMENT TYPE: Utility
PRIMARY EXAMINER: Benzion, Gary
NUMBER OF CLAIMS: 13
EXEMPLARY CLAIM: 1
LINE COUNT: 2172
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 23 OF 29 JICST-EPlus COPYRIGHT 2001 JST
TI Primary Structure of 6.5k-Arginine/Glutamate-rich Polypeptide from the Seeds of Sponge Gourd (Luffa cylindrica).
AB The amino acid sequence of 6.5k-arginine/glutamate rich polypeptide (6.5k-AGRP) from the seeds of sponge gourd (Luffa cylindrica) has been determined. The 6.5k-AGRP consists of a 47-residue polypeptide chain containing two disulfide bonds, and a molecular mass calculated to be 5695
Da, which fully coincides with a value of .cents.M + H!+= m/z 5693.39 obtained by matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF MS). The mass spectrometric evidence indicated that 6.5k-AGRP is also present partially truncated at the C-terminus. In our preparations, approximately half of the polypeptide molecules have the C-terminal sequence Arg-Arg-Glu-Val-Asp; the other half
lack Val-Asp and end with the glutamic acid, making a total of 45 residues
in the polypeptide chain. The two disulfide bonds connect Cys12 to Cys33 and Cys16 to Cys29. Comparison of the amino acid sequence of 6.5k-AGRP with those of the other known proteins included in the PIR protein sequence database showed that it is related to the amino acid sequence of the N-terminal region encoded by the first exon of the cocoa (**Theobroma cacao**) and cotton seeds **vicilin**
genes, sharing a characteristic two Cys-Xaa-Xaa-Xaa-Cys motif. (author abst.)

ACCESSION NUMBER: 970608797 JICST-EPlus
TITLE: Primary Structure of 6.5k-Arginine/Glutamate-rich Polypeptide from the Seeds of Sponge Gourd (Luffa cylindrica).
AUTHOR: KIMURA M; PARK S-S; SAKAI R; YAMASAKI N; FUNATSU G
CORPORATE SOURCE: Kyushu Univ., Fukuoka, JPN
SOURCE: Biosci Biotechnol Biochem, (1997) vol. 61, no. 6, pp. 984-988. Journal Code: G0021A (Fig. 6, Ref. 17)
CODEN: BBBIEJ; ISSN: 0916-8451
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article
LANGUAGE: English
STATUS: New

L4 ANSWER 24 OF 29 FSTA COPYRIGHT 2001 IFIS
TI Expression of the major bean proteins from **Theobroma cacao** (cocoa) in the yeasts Hansenula polymorpha and Saccharomyces cerevisiae.
AB Production of recombinant forms of the major proteins from the cocoa bean in 2 yeast expression systems is described. 3 major protein species are

found in the cocoa bean: an albumin of molecular mass 21 kDa (p21) and 2 insoluble **vicilin**-like proteins of molecular mass 31 and 47 kDa (p31 and p47, respectively). p31 and p47 are derived from a common 67-kDa precursor (p67) by post-translational processing. p21 and p67 coding sequences were expressed in Hansenula polymorpha using the methanol oxidase (MOX) promoter and in Saccharomyces cerevisiae using the pyruvate kinase (PYK) promoter. Expression constructs contained the native plant signal sequence, or various yeast signals. The p21 protein was successfully expressed and secreted from both yeasts with yields of approx. 50 mg/l. Production of the insoluble p67 protein proved more difficult; species of the correct molecular mass were recovered internally and small amounts of p47 were secreted using a yeast leader sequence. However, proteolytic cleavage led to the appearance of other secreted proteins of 28 and 18 kDa. [From En summ.] (KAR)

ACCESSION NUMBER: 96(08):B0017 FSTA FS FSTA
TITLE: Expression of the major bean proteins from **Theobroma cacao** (cocoa) in the yeasts Hansenula polymorpha and Saccharomyces cerevisiae.
AUTHOR: Yavuz, M. O.; Ashton, S. M. V.; Deakin, E. D.; Spencer, M. E.; Sudbery, P. E.
CORPORATE SOURCE: Correspondence (Reprint) address, P. E. Sudbery, Dep. of Molecular Biol. & Biotech., Univ. of Sheffield, Western Bank, Sheffield S10 2TN, UK
SOURCE: Journal of Biotechnology, (1996) 46 (1) 43-54, 23 ref.
ISSN: 0168-1656.
DOCUMENT TYPE: Journal
LANGUAGE: English

L4 ANSWER 25 OF 29 FSTA COPYRIGHT 2001 IFIS
TI A model for **vicilin** solubility at mild acidic pH, based on homology modelling and electrostatics calculations.
AB Cocoa (**Theobroma cacao**) storage protein is a member of the **vicilin** subclass of globulins. Hydrolysis of this protein is responsible for the formation of flavour peptides during fermentation of cocoa beans. Crystallographic structures of jack bean canavalin and French bean phaseolin were used to construct a homology model of the storage **vicilin** of cocoa. This work was undertaken to provide a molecular basis for the understanding of specific proteolysis in the protein monomer. Observations concerning the solubility of cocoa **vicilin**, its pH dependence and electrostatic interactions, made with reference to the homology model, are presented. Reported mol. wt. of protein subunits correlated with proteolysis at the site of a large hydrophilic insert in the mature protein. Burial of the hydrophobic amino acids on trimer formation was observed; this is a strongly conserved feature in the **vicilin** family. Histidine residues at the monomer-monomer interfaces of the trimer may contribute to the decreased solubility of cocoa **vicilin** at mild acidic pH - this is generally considered to be caused solely by aggregation near to the isoelectric point. Electrostatic calculations suggested that such an arrangement of histidine residues in the absence of specific counterion binding will not favour the particular geometry of trimer formation below neutral pH. It is proposed that these observations may assist in an understanding of the pH and ionic strength dependence of **vicilin** solubility in vitro, and possibly the behaviour of vicilins in the seed storage environment. [From En summ.] (KAR)

ACCESSION NUMBER: 96(06):K0003 FSTA FS FSTA
TITLE: A model for **vicilin** solubility at mild

acidic pH, based on homology modelling and electrostatics calculations.

AUTHOR: Warwicker, J.; O'Connor, J.
CORPORATE SOURCE: Protein Eng. Dep., Inst. of Food Res., Reading Lab., Earley Gate, Whiteknights Rd., Reading RG6 6BZ, UK
SOURCE: Protein Engineering, (1995) 8 (12) 1243-1251, 41 ref.
DOCUMENT TYPE: Journal
LANGUAGE: English

L4 ANSWER 26 OF 29 FSTA COPYRIGHT 2001 IFIS
TI The major seed proteins of **Theobroma cacao** L.
AB [The major seed proteins of **Theobroma cacao** (cocoa) were investigated, in order to classify those seed proteins from which the cocoa-specific flavour precursors might be derived.] Differential extractions of proteins from cocoa beans revealed the presence of an albumin fraction and a globulin fraction with proportions of 52 and 43%, respectively, of total seed proteins. No prolamin was detected. The glutelin fraction was found to consist of residual globulin. After fermentation, the first step in cocoa processing, the proportion of the globulin fraction was considerably reduced. The major albumin was a polypeptide with an apparent mol. wt. of 19 kDa. The globulin fraction contained polypeptides with apparent mol. wt. of 47, 31 and 14.5 kDa. Globulin prepared in the absence of the aspartyl proteinase inhibitor pepstatin contained 2 additional polypeptides with apparent mol. wt. of 28 and 16 kDa, respectively. The negative globulin of T. cacao was a glycoprotein with a sedimentation coeff. of 7-8S and a mol. wt. of 150 kDa. Its subunits were not cross-linked by disulphide bridges, in contrast to the legumin-like storage globulins which are predominant in the seeds of all other dicotyledons. Therefore, T. cacao is the first plant described to date whose seeds contained a **vicilin**-like globulin, but apparently no legumin-class globulin. (AS(HAB))
ACCESSION NUMBER: 93(08):K0001 FSTA FS FSTA
TITLE: The major seed proteins of **Theobroma cacao** L.
AUTHOR: Voigt, J.; Biehl, B.; Kamaruddin Syed Wazir, S.
CORPORATE SOURCE: Bot. Inst., Tech. Univ. Braunschweig, W-3300 Braunschweig, Germany
SOURCE: Food Chemistry, (1993) 47 (2) 145-151, 32 ref. ISSN: 0308-8146.
DOCUMENT TYPE: Journal
LANGUAGE: English

L4 ANSWER 27 OF 29 FSTA COPYRIGHT 2001 IFIS
TI Cloning and sequencing of a cDNA encoding the major storage proteins of **Theobroma cacao**. Identification of the proteins as members of the **vicilin** class of storage proteins.
AB The major storage proteins, polypeptides of 31 and 47 kDa, from cocoa seeds (**Theobroma cacao** L.), were identified and partially purified by preparative gel electrophoresis. The polypeptides were both N-terminally blocked, but some N-terminal amino-acid sequence was obtained from a cyanogen bromide peptide common to both polypeptides, permitting the construction of an oligonucleotide probe. This probe was used to isolate the corresponding copy-DNA (cDNA) clone from a library made from poly(A)+RNA from immature cocoa beans. The cDNA sequence has a single major open reading frame, that translates to give a 566-amino-acid polypeptide of Mr 65612. The existence of a common precursor to the 31- and 47-kDa polypeptides of this size was confirmed by immunoprecipitation from total poly(A)+RNA translation products. The precursor has an N-terminal hydrophobic sequence which appears to be a typical signal sequence, with a predicted site of cleavage 20 amino acids after the start. This is followed by a very hydrophilic domain of approx. 110 amino

acids, very rich in glutamine and charged residues (especially glutamate), and contains several Cys-X-X-X-Cys motifs. The cyanogen-bromide peptide common to the 47-kDa and 31-kDA polypeptides is very close to the proposed start of the mature domain, indicating that the 31-kDa polypeptide arises via further C-terminal processing. The polypeptide sequence is homologous to sequences of the **vicilin** class of storage proteins. [From En summ.] (VJG)

ACCESSION NUMBER: 93(02):K0004 FSTA FS FSTA
TITLE: Cloning and sequencing of a cDNA encoding the major storage proteins of **Theobroma cacao** . Identification of the proteins as members of the **vicilin** class of storage proteins.
AUTHOR: Spencer, M. E.; Hodge, R.
CORPORATE SOURCE: Plant Science Ltd., Firth Court, Sheffield Univ., Western Bank, Sheffield S10 2TN, UK
SOURCE: Planta, (1992) 186 (4) 567-576, 29 ref.
ISSN: 0032-0935.
DOCUMENT TYPE: Journal
LANGUAGE: English

L4 ANSWER 28 OF 29 FSTA COPYRIGHT 2001 IFIS
TI Comparison of the structure and nucleotide sequences of **vicilin** genes of cocoa and cotton raise questions about **vicilin** evolution.
AB **Vicilin** is a seed storage protein in cocoa (**Theobroma cacao**), and it may be an important flavour precursor in chocolate. The nucleotide sequence of the cocoa **vicilin** gene was characterized and compared with **vicilin** genes in cottonseed, with particular emphasis on the number of introns present in the cottonseed and cocoa genes (4 and 5, resp.). Implications for the likely evolutionary development of the spp. are discussed. (KAR)

ACCESSION NUMBER: 92(09):K0003 FSTA FS FSTA
TITLE: Comparison of the structure and nucleotide sequences of **vicilin** genes of cocoa and cotton raise questions about **vicilin** evolution.
AUTHOR: McHenry, L.; Fritz, P. J.
CORPORATE SOURCE: Correspondence (Reprint) address, P. J. Fritz, Dep. of Food Sci., Pennsylvania State Univ., Univ. Park, PA 16802, USA
SOURCE: Plant Molecular Biology, (1992) 18 (6) 1173-1176, 12 ref.
ISSN: 0167-4412.
DOCUMENT TYPE: Journal
LANGUAGE: English

L4 ANSWER 29 OF 29 FROSTI COPYRIGHT 2001 LFRA
TI The major seed proteins of **Theobroma cacao** L.
AN 319957 FROSTI
AB The storage proteins of **Theobroma cacao** seem to be important with respect to the formation of the cocoa-specific flavour. The major seed proteins of this plant were therefore investigated to classify those seed proteins from which cocoa-specific flavour precursors could be derived. Differential extractions have revealed the presence of an albumin fraction (52%) and a globulin fraction (43%) of total seed proteins. After fermentation the proportion of the globulin fraction is considerably reduced. The identified albumin and globulin classes are discussed. These seeds contain a **vicilin**-like globulin about

apparently no legumin-class globulin. Therefore the flavour-related peptides that are formed during fermentation and are assumed to be responsible for the formation of cocoa-specific components during roasting seem to be formed by proteolytic digestion of the cocoa **vicilin**.

TITLE: The major seed proteins of **Theobroma cacao** L.
AUTHOR: Voigt J.; Biehl B.; Wazir S.K.S.
SOURCE: Food Chemistry, 1993, 47 (2), 145-151 (32 ref.)
DOCUMENT TYPE: Journal
LANGUAGE: English
SUMMARY LANGUAGE: English